

[illegible]

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XX (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Agarwal P, Kabnick KS, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
XX WPI: 2001-536566/59.
DR N-PSDB; AAD16347.
XX
PT New secreted and membrane associated polypeptides for treating
PT Alzheimer's disease, psoriasis, cancer, enterocolitis, sleep and sexual
PT disorders, stroke, and asthma -
XX
PS Claim 1: Page 58-59; 94pp; English.
XX
CC The present sequence is a human sbhgcta protein,
CC a secreted protein of the invention.
CC The invention relates to secreted and membrane associated polypeptides
CC and nucleic acid molecules encoding such polypeptides. Sequences of the
CC invention are useful for treating diseases such as Alzheimer's disease,
CC amyotrophic lateral sclerosis (ALS), Zollinger-Ellison syndrome, diseases
CC of the immune system, haematopoietic disease, inflammation, anxiety,
CC schizophrenia, feeding disorders, anorexia, depression, social, sexual
CC and rewarded behaviour, cardiovascular disease, sleep disorder, learning
CC and memory alteration and altered immune response, seizure, migraine,
CC cancer, stroke, asthma, neuropathy, aging, sexual disorders, treatment
CC of transsexuals, growth abnormalities, obesity, infections, autoimmune
CC diseases (e.g. rheumatoid arthritis), cataractogenesis, angiogenesis,
CC disorders associated with healthy maintenance of gastric mucosa and
CC repair of acute and chronic mucosal lesion, lung carcinoma, cerebral
CC ischaemia, atherosclerosis, cirrhosis, Huntington's disease, headache,
CC amaemia, multiple sclerosis, Hodgson's disease, dilated cardiomyopathy,
CC congestive heart failure, cardiac arrhythmias, hypercholesterolaemia,
CC viral and non-viral hepatitis, type I and type II diabetes mellitus,
CC glomerulonephritis, renovascular hypertension, hypoglycaemia, periodic
CC paralyses, tendinitis and malignant hypertension. Polypeptides of the
CC invention are used to identify membrane bound and soluble receptors.
CC They are also useful as vaccines for inducing an immunological response
CC in a mammal. Polynucleotides of the invention are used in gene therapy.
CC They are also valuable for chromosome localisation studies and tissue
CC expression studies.
XX
SQ Sequence 130 AA:

```

Query Match 100.0%; Score 722; DB 22; Length 130;
 Best Local Similarity 100.0%; Pred. No. 9.1e-70;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MKLAEFLGPMALLLAGYGVLAGSSGNLRTFVGCAVREFTFLAKKPGCGRLRTTDDAC 60
   |||
DB 1 mklaefllgpmallllagyscvlgassgnlrlfvgcavrefflakpgcrglrlttddc 60
QY 61 WGRCTEWKPILEPPIYEAHHRVCTYNETKQYTVKLPNCAGVDPFYTYPAVAIRDCGAC 120
   |||
DB 61 wgrctewkpiileppyieahhrvctyneckytklpncagvpdftyypvaairdcgac 120
QY 121 STATTECETI 130
   |||
DB 121 stattececi 130

```

RESULT 2
 AAG63211
 ID AAG63211 standard; Protein; 130 AA.
 AC AAG63211;
 DT 01-OCT-2001 (first entry)
 XX Amino acid sequence of a human cystine knot polypeptide.
 DE Cystine knot polypeptide; follicular arrest; recruitment modulator;
 KW

```

KW fertility-related disorder; contraception; menopause; contraceptive;
KW follicle growth.
XX
OS Homo sapiens.
XX
PN WO200153346-A1.
XX
PD 26-JUL-2001.
XX
PF 17-JAN-2001; 2001WO-EP00570.
XX
PR 18-JAN-2000; 2000EP-0200185.
XX
PA (ALKU ) AKZO NOBEL NV.
XX
PI Mosselman S, Spek Van Der Pij;
XX
XX WPI: 2001-476102/51.
XX
DR N-PSDB; AAH42567.
XX
PT New DNA sequences, useful for coding or producing cystine knot
PT polypeptides, which are useful in preparing a pharmaceutical for
PT fertility-related disorders or contraception, and for controlling
PT follicular arrest and recruitment -
XX
PS Example 1: Page 23-24; 29pp; English.
XX
CC The present sequence represents a human cystine knot polypeptide. The
CC polypeptide is a follicular arrest and recruitment modulator. Cystine
CC knot polypeptides are useful in preparing a pharmaceutical for
CC fertility-related disorders or in contraception. The polypeptide is
CC particularly useful for controlling follicular arrest and recruitment.
CC Inhibition of recruitment can be used to delay (premature) menopause or
CC as a contraceptive. The polypeptide is also useful for in vitro
CC maturation and growth of follicles, e.g. from frozen ovarian tissue.
XX
SQ Sequence 130 AA:

```

Query Match 100.0%; Score 722; DB 22; Length 130;
 Best Local Similarity 100.0%; Pred. No. 9.1e-70;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MKLAEFLGPMALLLAGYGVLAGSSGNLRTFVGCAVREFTFLAKKPGCGRLRTTDDAC 60
   |||
DB 1 mklaefllgpmallllagyscvlgassgnlrlfvgcavrefflakpgcrglrlttddc 60
QY 61 WGRCTEWKPILEPPIYEAHHRVCTYNETKQYTVKLPNCAGVDPFYTYPAVAIRDCGAC 120
   |||
DB 61 wgrctewkpiileppyieahhrvctyneckytklpncagvpdftyypvaairdcgac 120
QY 121 STATTECETI 130
   |||
DB 121 stattececi 130

```

RESULT 3
 AAG64064
 ID AAG64064 standard; protein; 130 AA.
 AC AAG64064;
 DT 17-SEP-2001 (first entry)
 XX Human anterior pituitary hormone-related polypeptide.
 DE Human anterior pituitary hormone; hypertension; autoimmune disease;
 KW heart failure.
 OS Homo sapiens.
 DE Homo sapiens.
 KW WO200144475-A1.
 PN

PD 21-JUN-2001.
XX
PF 15-DEC-2000; 2000WO-JP08896.
XX
PR 17-DEC-1999; 99JP-0358707.
PR 18-FEB-2000; 2000JP-0046825.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Hinuma S, Fukusumi S, Fujii R, Hosoya M;
XX
DR WPI; 2001-408485/43.
DR N-PSDB; AAH46586.
XX
PT Polypeptides for treatment of hypertension, autoimmune disease and
XX heart failure
XX
PS Claim 1; Fig 2; 107pp; Japanese.
XX
CC The invention relates to a novel polypeptide comprising a fully defined
CC 130 amino acid sequence given in the specification and its amides,
CC esters and salts. The polypeptide has anterior pituitary hormone-related
CC activity. It is useful for the treatment of hypertension, autoimmune
CC diseases and heart failure. The screening method and kit also
CC provided in the invention are useful for identifying new substances
CC for treating and preventing these diseases. The present sequence is
CC the polypeptide of the invention.
XX
SQ Sequence 130 AA;

Query Match 100.0%; Score 722; DB 22; Length 130;
Best Local Similarity 100.0%; Pred. No. 9.1e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLAFLFGPMALLLAGYGCVLGASSGNLRTFVGCAVREFTFLAKKPGCGRLRTTDDAC 60
Db 1 mklafllfgpmallllagycvlgassgnlrtfvgcavreflflakkgpcrgrlrttddac 60
QY 61 WGRGETWEKPILEPPYIEAHHRVCTYNETKQVTKLPNCARGVDPFTTYPAATCDGAC 120
Db 61 wgrcetwekpileppyieahhrvctyнетkqvtklpncargvdpfttypaatcdcgac 120
QY 121 STATTECETI 130
Db 121 statteecti 130

RESULT 4

ID AAB84998 standard; Protein; 230 AA.

XX AAB84998;

XX 06-AUG-2001 (first entry)

XX Human novel gonadotropin (NOVGON) protein.

KW NOVG; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;
KW gonadotropin-like protein; NOVGON; interleukin-1; NOVINTRA; human;
KW cytosolic; neuroprotective; reproductive; antiinflammatory; cancer;
KW antibacterial; cerebroprotective; antidiabetic; antiarthritic;
KW antiasthmatic; antiallergic.

XX Homo sapiens.

XX MO200140291-A2.

XX 07-JUN-2001.

XX 06-DEC-2000; 2000WO-US33029.

XX 06-DEC-1999; 99US-0169056.

PR 09-DEC-1999; 99US-0169866.
PR 09-DEC-1999; 99US-0169886.
PR 10-DEC-1999; 99US-0170252.
PR 12-JAN-2000; 2000US-0175740.
PR 03-DEC-2000; 2000US-0170252.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Burgess CE, Prayaga SK, Shimkets RA, Rastelli L, Zernhusen BD;
PI Mezes PS;
XX
DR WPI; 2001-374790/39.
DR N-PSDB; AAF83867.
XX
PT Novel isolated human transmembrane, neuromedin peptide
PT gonadotropin-like protein and interleukin-1 receptor antagonist
PT proteins, useful for treating cancer, immune response disorder,
PT metabolic function disorders
XX
PS Claim 1; Fig 6B; 138pp; English.

CC The invention provides novel polypeptides (NOVG) selected from human
CC transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),
CC gonadotropin-like protein (NOVGON) and two interleukin-1 receptor
CC antagonist proteins (NOVINTRA A and B). The invention also provides
CC methods in which a NOVG polypeptide, polynucleotide and antibody are
CC used in the detection, prevention and treatment of a broad range of
CC pathological states. NOVTRAN can be used to treat is a cell signaling
CC disorder such as cancer, immune response disorder, hematopoietic
CC disorder, neurodegenerative disorder. NOVNEUR can be used to treat
CC endocrine disorder, muscle disorder, neurologic disorder, cancers of
CC central nervous system, breast, colon, ovary, kidney, prostate and
CC thyroid. NOVGON can be used to treat reproductive development disorder,
CC metabolic function disorder and melanoma. NOVINTRA A and B can be used
CC to treat bone metabolism or structure disorder, inflammatory response
CC disorder, immune regulation disorder, septic shock, stroke, diabetes,
CC arthritis and cancer. The present sequence represents the NOVGON
CC polypeptide.

SQ Sequence 230 AA;

Query Match 96.8%; Score 699; DB 22; Length 230;
Best Local Similarity 100.0%; Pred. No. 5.2e-67;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLAFLFGPMALLLAGYGCVLGASSGNLRTFVGCAVREFTFLAKKPGCGRLRTTDDAC 60
Db 1 mklafllfgpmallllagycvlgassgnlrtfvgcavreflflakkgpcrgrlrttddac 60

QY 61 WGRGETWEKPILEPPYIEAHHRVCTYNETKQVTKLPNCARGVDPFTTYPAATCDGAC 120
Db 61 wgrcetwekpileppyieahhrvctyнетkqvtklpncargvdpfttypaatcdcgac 120

QY 121 STATTE 126
Db 121 statte 126

XX 17-SEP-2001 (first entry)

XX Rat anterior pituitary hormone-related polypeptide #1.

KW Rat; anterior pituitary hormone; hypertension; autoimmune disease;
KW heart failure.
XX
XX Ratus sp.

XX AAG64067;

XX 17-SEP-2001 (first entry)

XX Rat anterior pituitary hormone-related polypeptide #1.

XX Rat; anterior pituitary hormone; hypertension; autoimmune disease;
KW heart failure.

XX Ratus sp.

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XX MO200144475-A1.
PN
XX
XX 21-JUN-2001.
PD
XX
XX 15-DEC-2000; 2000WO-JP08896.
PE
XX 17-DEC-1999; 99JP-0358707.
PR 18-FEB-2000; 2000JP-0046825.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX
XX Hinuma S, Fukusumi S, Fujii R, Hosoya M;
PI
XX WPI; 2001-408485/43.
DR
XX N-PSDB; AAH46593.
XX
XX Polypeptides for treatment of hypertension, autoimmune disease and
PT heart failure -
XX
XX Claim 2; Page 102-103; 107pp; Japanese.
PS
XX
XX The invention relates to a novel polypeptide comprising a fully defined
CC 130 amino acid sequence given in the specification and its amides,
CC esters and salts. The polypeptide has anterior pituitary hormone-related
CC activity. It is useful for the treatment of hypertension, autoimmune
CC diseases and heart failure. The screening method and kit also
CC provided in the invention are useful for identifying new substances
CC for treating and preventing these diseases. The present sequence is
CC is a polypeptide provided in the specification.
XX
XX Sequence 129 AA:
SQ
Query Match 85.2%; Score 615.5; DB 22; Length 129;
Best Local Similarity 85.4%; Pred. No. 2.4e-58;
Matches 111; Conservative 8; Mismatches 10; Indels 1; Gaps 1;
QY 1 MKIAFLFLGPMALLLAGYGVLAGSSGNLRFTVGCANREFTFLAKKPGRCGLRITTDAC 60
DB 1 mklvlylvlg-taalllgdsdsvlsssgnlhftvgcavreflftvakkgpcrglrittdac 59
QY 61 WGRCEIWEKPIIEPPIIEAHHRVCTIETKQYTKLPNCAPGVDPFYTPVAIRDCGAC 120
DB 60 wgrcetwexkplieppyleahhrvctyetrivtklpncapgvdpfitypmavrcdcgac 119
QY 121 STATEECETI 130
DB 120 stateeceti 129
RESULT 6
AAG64065
ID AAG64065 standard; Protein; 106 AA.
XX
XX AAG64065;
AC
XX
XX 17-SEP-2001 (first entry)
DT
XX
XX Human anterior pituitary hormone-related polypeptide #2.
DE
XX
XX Human; anterior pituitary hormone; hypertension; autoimmune disease;
KW heart failure.
XX
XX Homo sapiens.
OS
XX
XX WO200144475-A1.
PN
XX
XX 21-JUN-2001.
PD
XX
XX 15-DEC-2000; 2000WO-JP08896.
PE
XX
XX 17-DEC-1999; 99JP-0358707.
PR
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PR 18-FEB-2000; 2000JP-0046825.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX
XX Hinuma S, Fukusumi S, Fujii R, Hosoya M;
PI
XX
XX WPI; 2001-408485/43.
DR
XX N-PSDB; AAH46589.
XX
XX Polypeptides for treatment of hypertension, autoimmune disease and
PT heart failure -
XX
XX Claim 3; Page 100; 107pp; Japanese.
PS
XX
XX The invention relates to a novel polypeptide comprising a fully defined
CC 130 amino acid sequence given in the specification and its amides,
CC esters and salts. The polypeptide has anterior pituitary hormone-related
CC activity. It is useful for the treatment of hypertension, autoimmune
CC diseases and heart failure. The screening method and kit also
CC provided in the invention are useful for identifying new substances
CC for treating and preventing these diseases. The present sequence is
CC is a polypeptide of the invention.
XX
XX Sequence 106 AA:
SQ
Query Match 83.1%; Score 600; DB 22; Length 106;
Best Local Similarity 100.0%; Pred. No. 9e-57;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 ASSGNLRFTVGCANREFTFLAKKPGRCGLRITTDACWRCETWEKPIIEAHHRVC 84
DB 1 assgnlrftvgcavreflftlakkgpcrglrittdacwrcetwexkpliepyleahhrvc 60
QY 85 TYNETKQYTKLPNCAPGVDPFYTPVAIRDCGACSTATEECETI 130
DB 61 tynektqytklpncapgvdpfitypvairdcgacstateeceti 106
RESULT 7
AAG64068
ID AAG64068 standard; Protein; 106 AA.
XX
XX AAG64068;
AC
XX
XX 17-SEP-2001 (first entry)
DT
XX
XX Rat anterior pituitary hormone-related polypeptide #2.
DE
XX
XX Rat; anterior pituitary hormone; hypertension; autoimmune disease;
KW heart failure.
XX
XX Rattus sp.
OS
XX
XX WO200144475-A1.
PN
XX
XX 21-JUN-2001.
PD
XX
XX 15-DEC-2000; 2000WO-JP08896.
PE
XX
XX 17-DEC-1999; 99JP-0358707.
PR 18-FEB-2000; 2000JP-0046825.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX
XX Hinuma S, Fukusumi S, Fujii R, Hosoya M;
PI
XX
XX WPI; 2001-408485/43.
DR
XX N-PSDB; AAH46594.
XX
XX Polypeptides for treatment of hypertension, autoimmune disease and
PT heart failure -
XX
```

PS Claim 4; Page 104; 107pp; Japanese.
 CC The invention relates to a novel polypeptide comprising a fully defined
 CC 130 amino acid sequence given in the specification and its amides,
 CC esters and salts. The polypeptide has anterior pituitary hormone-related
 CC activity. It is useful for the treatment of hypertension, autoimmune
 CC diseases and heart failure. The screening method and kit also
 CC provided in the invention are useful for identifying new substances
 CC for treating and preventing these diseases. The present sequence is
 CC is a polypeptide provided in the specification.
 XX Sequence 106 AA;
 SO
 Query Match 79.2%; Score 572; DB 22; Length 106;
 Best Local Similarity 92.5%; Pred. No. 9.1e-54;
 Matches 98; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
 QY 25 ASSGNLRTFVGCAVREFTFLAKKPGCGRLRTTDCACGRCETWEKPILEPPYIEAHNRVC 84
 DB 1 sssgnlhtfvgcavreflftakpqcrglritldacwgcetwepkllpeyyiaeyhrvc 60
 QY 85 TYNETKQVTVLTPNCAPGVDPFYTTPVAIRDCGACGSTRTECEFI 130
 DB 61 tynekrvtvkllpncapgvdpfytppmavrcdcgacstattecefi 106
 RESULT 8
 AAG63212
 ID AAG63212 standard; Protein; 75 AA.
 AC AAG63212;
 XX
 DT 01-OCT-2001 (first entry)
 XX
 DE Amino acid sequence of human cystine knot polypeptide splice variant.
 DE
 KW Cystine knot polypeptide; follicular arrest; recruitment modulator;
 KW fertility-related disorder; contraception; menopause; contraceptive;
 KW follicle growth.
 XX
 OS Homo sapiens.
 XX
 PN WO200153346-A1.
 PD
 XX 26-JUL-2001.
 PF 17-JAN-2001; 2001WO-EP00570.
 XX
 PR 18-JAN-2000; 2000EP-0200185.
 XX
 PA (ALKU) AKZO NOBEL NV.
 XX
 PI Mosseelman S, Spek Van Der PJ;
 XX
 DR WPI: 2001-476102/51.
 DR N-PSDB; AAH42568.
 XX
 PT New DNA sequences, useful for coding or producing cystine knot
 PT polypeptides, which are useful in preparing a pharmaceutical for
 PT fertility-related disorders or contraception, and for controlling
 PT follicular arrest and recruitment -
 XX
 PS Example 1; Page 25; 29pp; English.
 XX
 CC The present sequence represents a human cystine knot polypeptide splice
 CC variant. The polypeptide is a follicular arrest and recruitment
 CC modulator. Cystine knot polypeptides are useful in preparing a
 CC pharmaceutical for fertility-related disorders or in contraception.
 CC The polypeptide is particularly useful for controlling follicular
 CC arrest and recruitment. Inhibition of recruitment can be used to delay
 CC (premature) menopause or as a contraceptive. The polypeptide is also
 CC useful for in vitro maturation and growth of follicles, e.g. from

CC frozen ovarian tissue.
 XX
 SO Sequence 75 AA;
 QY
 DB 61 WGRCEWE 68
 DB 61 wgrcetwe 68
 Query Match 51.2%; Score 370; DB 22; Length 75;
 Best Local Similarity 100.0%; Pred. No. 3e-32;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLAEFLFGPVALLLLAGYCVLGASSGNLRTFVGCAVREFTFLAKKPGCGRLRTTDCAC 60
 DB 1 mklaeflfgpvallllagycvlgassgnlritfvgcavreflftakpqcrglritldac 60
 QY
 DB 61 wgrcetwe 68
 DB 61 wgrcetwe 68
 RESULT 9
 AAB71792
 ID AAB71792 standard; protein; 141 AA.
 AC AAB71792;
 XX
 DT 02-MAY-2001 (first entry)
 XX
 DE Bovine luteotropin beta-chain precursor.
 DE
 KW Bovine; luteotropin; beta-human chorionic gonadotropin; beta-hCG; anti-HIV;
 KW cytostatic; antianaemic; vascular; osteopathic; antiinflammatory;
 KW gene therapy; maternin; MA peptide; pMA peptide;
 KW human immunodeficiency virus; HIV; cancer; wasting disorder;
 KW haematopoietic disorder; inflammation; angiogenic disorder.
 XX
 OS Bos sp.
 XX
 PN WO200110907-A2.
 PD
 XX 15-FEB-2001.
 PF 05-AUG-2000; 2000WO-US21495.
 XX
 PR 06-AUG-1999; 99US-0147825.
 PR 13-MAR-2000; 2000US-0188777.
 XX
 PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 XX
 PI Gallo R, Bryant J, Lunardi-Iskandar Y, Powell R, Reitz M;
 PI Foulke J, Lewis G;
 XX
 DR WPI: 2001-147510/15.
 XX
 PT Cells that produce therapeutic beta-human chorionic gonadotropin
 PT fragments, useful for the treatment of human immunodeficiency virus
 PT infections, cancers, wasting disorders, hematopoietic disorders,
 PT inflammation and angiogenic disorders -
 XX
 PS Disclosure; Page 26; 185pp; English.
 XX
 CC The present sequence is given in a specification relating to
 CC therapeutic polypeptides originally isolated from human early pregnancy
 CC urine, now synthetically produced, as well as functional equivalents of
 CC these polypeptides. Novel beta-human chorionic gonadotropin (hCG)
 CC fragments, designated Maternin (RTM) and referred to as MA and pMA
 CC peptides, are disclosed. Both native and synthetic MA inhibited growth
 CC of human tumour cells implanted into immuno-deficient mice by between 60
 CC to 100%, relative to control studies. The therapeutic MA polypeptides
 CC may be used for the prevention and treatment of a range of diseases and
 CC disorders, including human immunodeficiency virus (HIV) infections,
 CC cancers (especially Kaposi's sarcoma), wasting disorders, haematopoietic
 CC disorders (e.g. anaemias, radiation mediated bone marrow damage and
 CC trauma related blood loss), inflammation and angiogenic disorders.
 XX


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Db      61 -kepvfkspstvyqhvctyrdvyeitrlpdcppwvdphtvtyvalscdscloimctsd 119
OY      127 C 127
Db      120 c 120

RESULT 12
AAR15106
ID      AAR15106 standard; Protein: 145 AA.
AC      AAR15106;
XX
XX
DT      11-FEB-1992 (first entry)
XX
DE      hCG/BLH chimera, D10.
XX
XX      glycoprotein hormone; immuno-castration;
KW      immuno-contragestive; vaccine; human chorionic gonadotropin;
KM      luteinising hormone; LH; CG; bovine.
XX
OS      Homo sapiens.
OS      Bos taurus.
XX
XX      WC09116922-A.
XX
XX      14-NOV-1991.
XX
XX      PD
XX      PF      07-MAY-1991; 91WO-0503162.
XX
XX      PR      08-MAY-1990; 90US-0520703.
XX
XX      PA      (UYNE-) UNIV MED NEW JERSEY.
XX
XX      Campbell RK, Moyle WR;
XX
XX      WPI; 1991-353528/48.
XX
XX      DR
XX      PT      New glyco-protein hormone analogues - for inducing fertility as
PT      immuno-castration agents, for suppressing reproductive system
PT      development and as immuno-contragestive vaccines.
XX
XX      PS      Table IV; Page 63; 94pp; English.
XX
XX      CC      The sequence is an analogue of mature hCG beta subunit having
CC      several residues replaced by the corresponding residues in the
CC      bovine LH protein. The chimeric hormone may be useful for identify-
CC      ing residues which are important for binding to the human receptor
CC      and may also have applications as an immunogen, agonist and/or
CC      antagonist.
CC      See AAR15043, AAR15061-R15125 and AAR15161-R15198.
XX
XX      SQ      Sequence 145 AA;

Query Match      27.3%; Score 197; DB 12; Length 145;
Best Local Similarity 39.0%; Pred. No. 2.4e-13;
Matches 41; Conservative 18; Mismatches 38; Indels 8; Gaps 4;
```

```
AC      AAM47027;
XX
XX      DT      11-MAY-1998 (first entry)
XX
XX      DE      eCG hormone beta-subunit variant (1-131 amino acid residues).
XX
XX      KW      Equine; chorionic gonadotropin; hormone; eCG; beta-subunit; treatment;
KW      follicle-stimulating hormone; FSH; luteinising hormone; LH; ovulation;
KM      ovarian disease; variant.
XX
XX      OS      Family Equidae.
OS      Synthetic.
XX
XX      FH      Key
XX      FT      Peptide      Location/Qualifiers
XX      FT      1..20
XX      FT      /note= "signal peptide"
XX      FT      21..131
XX      FT      Protein      /note= "mature protein"
XX
XX      PN      JPI0036399-A.
XX
XX      PD      10-FEB-1998.
XX
XX      PF      24-JUL-1996; 96JP-0212197.
XX
XX      PR      24-JUL-1996; 96JP-0212197.
XX
XX      PA      (ELED ) DENKI KAGAKU KOGYO KK.
XX
XX      WPI; 1998-174916/16.
XX
XX      DR
XX      PT      Recombinant truncated equine chorionic gonadotropin hormone - has
PT      enhanced follicle-stimulating hormone activity and reduced
PT      luteinising hormone activity; useful as ovulation inducer
XX
XX      PS      Claim 7; Page -: 16pp; Japanese.
XX
XX      CC      This is a variant of the beta-subunit of an equine chorionic gonadotropin
CC      (eCG) hormone. The variants are created by removing 39 or lesser amino
CC      acid residues from the C-terminal peptide region of the beta-subunit. The
CC      recombinant eCG hormone is composed of alpha-subunit and the variant
CC      beta-subunits of eCG hormone and has a substantially enhanced follicle-
CC      stimulating hormone (FSH) activity and reduced luteinising hormone (LH)
CC      activity. The hormone is an ovulation inducer and can be used as an
CC      agent for the treatment of ovarian diseases.
CC      Note: This sequence does not appear in the specification. It has been
CC      created by modifying the eCG beta-subunit sequence provided in Page 11.
XX
XX      SQ      Sequence 131 AA;

Query Match      25.4%; Score 183.5; DB 19; Length 131;
Best Local Similarity 35.5%; Pred. No. 5.9e-12;
Matches 44; Conservative 15; Mismatches 48; Indels 17; Gaps 5;
```

XX	11-MAY-1998	(first entry)
DF		
DE	ecg hormone beta-subunit variant (1-134 amino acid residues).	
XX		
XX	Equine; chorionic gonadotropin; hormone; eCG; beta-subunit; treatment;	
KW	follicle-stimulating hormone; FSH; luteinising hormone; LH; ovulation;	
KW	ovarian disease; variant.	
XX		
OS	Family Equidae.	
OS	Synthetic.	
FT	Key	Location/Qualifiers
FT	Peptide	1..20
FT	Protein	/note= "signal peptide" 21..134 /note= "mature protein"
XX		
PN	JPI0036399-A.	
XX		
PD	10-FEB-1998.	
XX		
PF	24-JUL-1996;	96JP-0212197.
XX		
PR	24-JUL-1996;	96JP-0212197.
XX		
PA	(ELED) DENKI KAGAKU KOGYO KK.	
DR	WPI: 1998-174916/16.	
XX		
PT	Recombinant truncated equine chorionic gonadotropin hormone - has	
PT	enhanced follicle-stimulating hormone activity and reduced	
PT	luteinising hormone activity; useful as ovulation inducer	
XX		
PS	Claim 6; Page -: 16pp; Japanese.	
XX		
CC	This is a variant of the beta-subunit of an equine chorionic gonadotropin	
CC	(eCG) hormone. The variants are created by removing 39 or lesser amino	
CC	acid residues from the C-terminal peptide region of the beta-subunit. The	
CC	recombinant eCG hormone is composed of alpha-subunit and the variant	
CC	beta-subunits of eCG hormone and has a substantially enhanced follicle-	
CC	stimulating hormone (FSH) activity and reduced luteinising hormone (LH)	
CC	activity. The hormone is an ovulation inducer and can be used as an	
CC	agent for the treatment of ovarian diseases.	
CC	Note: This sequence does not appear in the specification. It has been	
CC	created by modifying the eCG beta-subunit sequence provided in Page 11.	
XX		
XX	Sequence 134 AA;	

Query Match	25.4%	Score 183.5	DB 19	Length 134
Best Local Similarity	35.5%	Pred. No. 6e-12		
Matches	44	Conservative 15	Mismatches 48	Indels 17
			Gaps	5

QY	11	MAILLIAGYCVLGA	SSGNLRTFVGC	CAVEEFPLAKKPGCR	-GLRIYTDACWGRCETWEK	69
		: :		: :	: :	:
Db	7	llwmllsvgyv-w	vsrglprlp--	crpinalaaek	eespcilftftscicg	yopsmr 63
						:
QY	70	-----PILEP	RYIEAHNRVCTY	NETKOYTKL	PNCAPGVDFYTY	PVAIRCDGCA
		: :				
Db	64	ympaalp	prpdp-----	vclyrelr	faslrlpgcp	pdpvmsvfpvalschgpcqik 116
QY	124	TTEC	127			
		:				
Db	117	tdc	120			

RESULT	15
AAW47026	
ID	AAW47026 standard; protein; 137 AA
XX	
AC	AAW47026;
XX	

DT	11-MAY-1998	(first entry)
XX		
DE	ecg hormone beta-subunit variant (1-137 amino acid residues) .	
XX		
KW	Equine; chorionic gonadotropin; hormone; ecg; beta-subunit; treatment;	
KW	follicle-stimulating hormone; FSH; luteinising hormone; LH; ovulation;	
XX	ovarian disease; variant.	
XX		
OS	Family Equidae.	
XX	Synthetic.	
XX		
XX	Key	Location/Qualifiers
FT	Peptide	1..20
FT		/note= "signal peptide"
FT	Protein	21..137
FT		/note= "mature protein"
XX		
PN	JP10036399-A.	
XX		
PD	10-FEB-1998.	
XX		
PF	24-JUL-1996;	96JP-0212197.
XX		
PR	24-JUL-1996;	96JP-0212197.
XX		
PA	(ELED) DENKI KAGAKU KOGYO KK.	
XX		
DR	WPI; 1998-174916/16.	
XX		
PT	Recombinant truncated equine chorionic gonadotropin hormone - has	
PT	enhanced follicle-stimulating hormone activity and reduced	
PT	luteinising hormone activity; useful as ovulation inducer	
XX		
XX		
PS	Claim 8; Page -: 16pp; Japanese.	
XX		
CC	This is a variant of the beta-subunit of an equine chorionic gonadotropin	
CC	(ecg) hormone. The variants are created by removing 39 or lesser amino	
CC	acid residues from the C-terminal peptide region of the beta-subunit. The	
CC	recombinant ecg hormone is composed of alpha-subunit and the variant	
CC	beta-subunits of ecg hormone and has a substantially enhanced follicle-	
CC	stimulating hormone (FSH) activity and reduced luteinising hormone (LH)	
CC	activity. The hormone is an ovulation inducer and can be used as an	
CC	agent for the treatment of ovarian diseases.	
CC	Note: This sequence does not appear in the specification. It has been	
CC	created by modifying the ecg beta-subunit sequence provided in Page 11.	
XX		
SO	Sequence 137 AA;	

```

Query Match          25.4%; Score 183.5; DB 19; Length 137;
Best Local Similarity 35.5%; Pred. No. 6,2e-12;
Matches 44; Conservative 15; Mismatches 48; Indels 17; Gaps 5;

QY 11 MALLLLAGYCVLGASSGNLRPTFGCAVAREFTFLAKKPGCR-GLRITTDACMGCEIWEK 69
   : : : : : | | | | | : : : : : | | | | : : : : :
Db 7 111mml1svgyv-wasrgplrp1--cprnatlaaekeapcliftfstsiaegyapsmvr 63
   : : : : : | | | | | : : : : : | | | | : : : : :

QY 70 -----PILEPPYIEAHHRVCTYNETKQYTVKLPNCAPGVDFEYTYPAAIRCDGAGCSTA 123
   : : : : : | | | | | : : : : : | | | | : : : : :
Db 64 vmpaalpripqp-----vclyrelrfasir1rlpcpgpvdpmvafpalischgpcq4ik 116
   : : : : : | | | | | : : : : : | | | | : : : : :

QY 124 TTEC 127
   : : : : : | | | | | : : : : : | | | | : : : : :
Db 117 tldc 120
   : : : : : | | | | | : : : : : | | | | : : : : :

```

Search completed: July 9, 2002, 13:34:00
Job time: 215 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OK protein - protein search, using sw model

Run on: July 9, 2002, 13:29:15 ; Search time 12.92 Seconds
(without alignments)
245,768 Million cell updates/sec

Title: US-09-723-970-1
Perfect score: 722
Sequence: 1 MKLAFLECPMALLLAGYG.....VAIRCDGACSFATTECERT 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues
Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : Issued_Patents_AA: *
1: /cgn2-6/ptodata/2/1aa/5A-COMB.pep: *
2: /cgn2-6/ptodata/2/1aa/5B-COMB.pep: *
3: /cgn2-6/ptodata/2/1aa/6A-COMB.pep: *
4: /cgn2-6/ptodata/2/1aa/6B-COMB.pep: *
5: /cgn2-6/ptodata/2/1aa/PTUS-COMB.pep: *
6: /cgn2-6/ptodata/2/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	178	24.7	149	1	US-08-425-673-5 Sequence 5, Appli
2	170	23.5	104	4	US-08-918-288-74 Sequence 74, Appl
3	170	23.5	104	4	US-09-282-357-74 Sequence 74, Appl
4	170	23.5	108	4	US-08-918-288-73 Sequence 73, Appl
5	170	23.5	108	4	US-09-282-357-73 Sequence 73, Appl
6	170	23.5	111	4	US-08-918-288-72 Sequence 72, Appl
7	170	23.5	111	4	US-09-282-357-72 Sequence 72, Appl
8	164	22.7	222	4	US-08-918-288-30 Sequence 30, Appl
9	164	22.7	222	4	US-09-282-357-30 Sequence 30, Appl
10	164	22.7	223	4	US-08-918-288-27 Sequence 27, Appl
11	164	22.7	223	4	US-09-282-357-27 Sequence 27, Appl
12	164	22.7	229	4	US-08-918-288-12 Sequence 12, Appl
13	164	22.7	229	4	US-09-282-357-12 Sequence 12, Appl
14	162	22.4	234	4	US-08-918-288-9 Sequence 9, Appli
15	162	22.4	234	4	US-09-282-357-9 Sequence 9, Appli
16	161	22.3	111	1	US-08-425-673-3 Sequence 3, Appli
17	161	22.3	111	1	US-08-425-673-4 Sequence 4, Appli
18	157	21.7	181	4	US-08-918-288-36 Sequence 36, Appl
19	157	21.7	181	4	US-09-282-357-36 Sequence 36, Appl
20	156	21.6	131	6	US-09-282-357-35 Patent No. 517193-3
21	155	21.5	114	4	US-08-918-288-71 Sequence 71, Appl
22	155	21.5	114	4	US-09-282-357-71 Sequence 71, Appl
23	155	21.5	234	4	US-08-918-288-6 Sequence 6, Appli
24	155	21.5	234	4	US-08-918-288-21 Sequence 21, Appl
25	155	21.5	234	4	US-08-918-288-24 Sequence 24, Appl
26	155	21.5	234	4	US-09-282-357-6 Sequence 6, Appli
27	155	21.5	234	4	US-09-282-357-21 Sequence 21, Appl

28	155	21.5	234	4	US-09-282-357-24 Sequence 24, Appl
29	155	21.5	237	4	US-08-918-288-18 Sequence 18, Appl
30	155	21.5	237	4	US-09-282-357-18 Sequence 18, Appl
31	155	21.5	265	4	US-08-918-288-3 Sequence 3, Appli
32	155	21.5	265	4	US-08-918-288-39 Sequence 39, Appl
33	155	21.5	265	4	US-09-282-357-3 Sequence 3, Appli
34	155	21.5	265	4	US-08-918-288-39 Sequence 39, Appl
35	152	21.1	165	2	US-08-709-924-2 Sequence 2, Appli
36	152	21.1	165	2	US-08-709-925-2 Sequence 2, Appli
37	152	21.1	165	4	US-08-709-948-2 Sequence 15, Appl
38	151	20.9	237	4	US-08-918-288-15 Sequence 15, Appl
39	151	20.9	237	4	US-09-282-357-15 Sequence 15, Appl
40	145.5	20.2	307	4	US-08-804-166-4 Sequence 4, Appli
41	145.5	20.2	307	4	US-08-910-991-4 Sequence 1, Appli
42	144	19.9	145	1	US-08-298-1898-1 Sequence 1, Appli
43	143	19.8	114	4	US-08-918-288-69 Sequence 69, Appl
44	143	19.8	114	4	US-09-282-357-69 Sequence 69, Appl
45	143	19.8	145	1	US-08-475-213-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-425-673-5
; Sequence 5, Application US/08425673
; Patent No. 5508261
GENERAL INFORMATION:
APPLICANT: Moyle, William R.
TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
TITLE OF INVENTION: Methods For Preparing and Using Same
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Richard R. Muccino
STREET: P.O. Box 1267
CITY: Princeton
STATE: New Jersey
COUNTRY: USA
ZIP: 08551
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,673
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/717,151
FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Muccino, Richard R.
REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UMD 1.0-004
TELEPHONE: (609) 466-3407
TELEFAX: (609) 466-2760
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-425-673-5
Query Match 24.7%; Score 178; DB 1; Length 149;
Best Local Similarity 35.8%; Pred. No. 2.1e-12;


```
? NUMBER OF SEQUENCES: 83
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: MORRISON & FOERSTER
? STREET: 2000 Pennsylvania Avenue, NW, suite 5500
? City: Washington
? STATE: DC
? COUNTRY: USA
? ZIP: 20006-1888
? COMPUTER READABLE FORM:
? MEDIUM TYPE: diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/918,288
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/282,357
? FILING DATE:
? APPLICATION NUMBER: 08/853,524
? FILING DATE: 09-MAY-1997
? APPLICATION NUMBER: 08/199,382
? FILING DATE: 18-FEB-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Murashige, Kate H
? REGISTRATION NUMBER: 29,959
? REFERENCE/DOCKET NUMBER: 29500-20050.25
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-887-1500
? TELEFAX: 202-887-0763
? TELEX:
? INFORMATION FOR SEQ ID NO: 73:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 108 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? US-08-918-288-73

Query Match      23.5%; Score 170; DB 4; Length 108;
Best Local Similarity 37.5%; Pred. No. 1.1e-11;
Matches 36; Conservative 14; Mismatches 38; Indels 8; Gaps 4;

QY 36 CAVREFFLAKKPCRCGLRITTDACW--GRCETWEKPILEP--PYIAHHRVCTYNETKQ 91
| : | : | | | | | : | : | : | : | : | : | : | : | : | : | : |
Db 3 CELNITITAVEKEGC-GFCITINTWCAGCYTRDLVYKDPARKIQ--KTCTFKELVY 58

QY 92 VTVKLPNCAGVDPFYYTPVAIRCDGACGASTATTEC 127
| : | | | | | | | | | | | | | | | : | : | : | : | : | : | : |
Db 59 ETVRVPGCAHHDLSLYTPVATQCHGCKGDSSTDC 94

RESULT 5
US-09-282-357-73
? Sequence 73, Application US/09282357
? Patent No. 6242580
? GENERAL INFORMATION:
? APPLICANT: BOYLE, Irving
? APPLICANT: MOYLE, William R.
? TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
? TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTER
? NUMBER OF SEQUENCES: 83
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: MORRISON & FOERSTER
? STREET: 2000 Pennsylvania Avenue, NW, suite 5500
? City: Washington
? STATE: DC
? COUNTRY: USA
? ZIP: 20006-1888
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
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? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/282,357
? FILING DATE:
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/918,288
? FILING DATE: 25 AUG-1997
? APPLICATION NUMBER: 08/853,524
? FILING DATE: 09-MAY-1997
? APPLICATION NUMBER: 08/199,382
? FILING DATE: 18-FEB-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Murashige, Kate H
? REGISTRATION NUMBER: 29,959
? REFERENCE/DOCKET NUMBER: 29500-20050.25
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-887-1500
? TELEFAX: 202-887-0763
? TELEX:
? INFORMATION FOR SEQ ID NO: 73:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 108 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? US-09-282-357-73

Query Match      23.5%; Score 170; DB 4; Length 108;
Best Local Similarity 37.5%; Pred. No. 1.1e-11;
Matches 36; Conservative 14; Mismatches 38; Indels 8; Gaps 4;

QY 36 CAVREFFLAKKPCRCGLRITTDACW--GRCETWEKPILEP--PYIAHHRVCTYNETKQ 91
| : | : | | | | | : | : | : | : | : | : | : | : | : | : | : |
Db 3 CELNITITAVEKEGC-GFCITINTWCAGCYTRDLVYKDPARKIQ--KTCTFKELVY 58

QY 92 VTVKLPNCAGVDPFYYTPVAIRCDGACGASTATTEC 127
| : | | | | | | | | | | | | | | | : | : | : | : | : | : | : |
Db 59 ETVRVPGCAHHDLSLYTPVATQCHGCKGDSSTDC 94

RESULT 6
US-08-918-288-72
? Sequence 72, Application US/08918288
? Patent No. 6238890
? GENERAL INFORMATION:
? APPLICANT: BOYLE, Irving
? APPLICANT: MOYLE, William R.
? TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
? TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTER
? NUMBER OF SEQUENCES: 83
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: MORRISON & FOERSTER
? STREET: 2000 Pennsylvania Avenue, NW, suite 5500
? City: Washington
? STATE: DC
? COUNTRY: USA
? ZIP: 20006-1888
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/918,288
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/282,357
? FILING DATE:
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36 CAVREFTFLAKKPGCR-GLRITTDACWGRCEETWEKPILEP--PYIEAHHRYCTYNETKOV 922

Db 78 TVRVPCGAHNDSTLYTPVATOCCHGCKDSDSTDC 112

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 9, 2002, 13:30:50 ; Search time 16.43 Seconds

Title: US-09-723-970-1

Sequence: 1 MKLAFLFLGPMALLLAGYG.....VAIRCDGACSTATTECETI 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	45 summaries

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Database : PIR_71:*
1: plr1:*
2: plr2:*
3: plr3:*
4: plr4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	210	29.1	141	1	UTBOB	lutropin beta chata
2	209	28.9	144	1	UTCAB	gonadotropin beta
3	207	28.7	141	1	B60626	gonadotropin beta
4	207	28.7	146	1	S16763	gonadotropin beta
5	204.5	28.3	141	1	UTSHB	lutropin beta chata
6	201.5	27.9	140	2	A48166	gonadotropin II be
7	201	27.8	142	1	C36179	gonadotropin II be
8	199	27.6	136	2	I50554	gonadotropin II be
9	198	27.4	133	2	S07092	gonadotropin II be
10	192	26.6	142	2	I51232	gonadotropin II be
11	189	26.2	112	2	S21196	lutropin beta chata
12	189	26.2	147	2	I50994	gonadotropin II be
13	186.5	25.8	142	2	I50143	gonadotropin II be
14	184	25.5	142	1	A25800	gonadotropin beta
15	183.5	25.4	169	1	KTHOB	choriogonadotropin
16	178	24.7	139	2	I52320	gonadotropin beta
17	178	24.7	141	1	UTRTB	testicular luteinini
18	175	24.2	141	2	JC4527	lutropin beta chata
19	174	24.1	118	1	FTTHOB	luteinizing hormom
20	174	24.1	141	1	UTPHB	folliotropin beta c
21	172.5	23.9	138	2	S00512	lutropin beta chata
22	168	23.3	147	2	S34148	thyrotropin beta c
23	165	22.9	118	2	PN0139	lutropin beta chata
24	164	22.9	128	2	S74085	lutropin beta chata
25	164	22.7	139	1	FTTHOB	folliotropin beta c
26	164	22.7	130	2	JC4526	folliotropin beta c
27	163	22.6	119	2	A61465	lutropin beta chata
28	163	22.6	130	2	A32893	folliotropin beta c
29	162	22.4	129	1	FTPHB	folliotropin beta c

30	162	22.4	141	1	UTRUB	Intropin beta chain
31	161	22.3	118	1	PNO141	Intropin beta chain
32	159	22.0	129	1	FTSHB	folitropin beta c
33	158	21.9	106	2	S74084	folitropin beta c
34	157.5	21.8	138	1	TPGCB	thyrotropin beta c
35	157	21.7	165	1	K7BAB	choriogonadotropin
36	155.5	21.5	113	2	S07216	Intropin beta chain
37	155	21.5	165	1	K7HUB	Intropin beta chain
38	154.5	21.4	138	1	UTRUB	thyrotropin beta c
39	154.5	21.4	147	2	A48194	thyrotropin beta c
40	154	21.3	129	2	A23550	folitropin beta c
41	154	21.3	138	1	TTBOB	Intropin beta c
42	153	21.2	137	2	B36179	gonadotropin I beta c
43	148.5	20.6	137	2	S34349	gonadotropin I beta c
44	148.5	20.6	138	2	A29479	thyrotropin beta c
45	146.5	20.3	137	2	I51231	gonadotropin I beta c

ALIGNMENTS

```

RESULT      1
UTRBOB
lutropin beta chain precursor - bovine
NAlternate names: Interstitial cell-stimulating hormone (ICSH) beta chain; lutealini
C.Species: Bos primigenius taurus (cattle)
C.Date: 30-Jun-1987 #sequence revision 30-Jun-1987 #text_change 24-Nov-1999
C.Accession: A92534; A92518; A91212; A01499
R.Virgin, J.B.; Silver, B.J.; Thomson, A.R.; Nilson, J.H.
J. Biol. Chem. 260, 7072-7077, 1985
A.Title: The gene for the beta subunit of bovine lutelutinizng hormone encodes a gonadotrophin-releasing hormone receptor type 1
A.Reference number: A92534; MUID:85207729
A.Accession: A92534
A.Molecule type: DNA
A.Residues: 1-141 <VIR>
A.Cross-references: GB:M11506; NID:g163298; PIDN:AAB59267.1; PID:g163299
R.Maurel, R.A.
J. Biol. Chem. 260, 4684-4687, 1985
A>Title: Analysis of several bovine lutropin beta subunit cDNAs reveals heterogeneity
A.Reference number: A92518; MUID:85182575
A.Accession: A92518
A.Molecule type: mRNA
A.Residues: 3-111,'S','113-141 <MAU>
A.Cross-references: GB:M10077; NID:g163300; PIDN:AAA30623.1; PID:g163301
R.Maguhn-Rogister, G.; Hennem, G.
Eur. J. Biochem. 39, 235-253, 1973
A>Title: Lutetizing hormone. The primary structures of the beta-subunit from bovine
A.Reference number: A91212; MUID:74075724
A.Accession: A91212
A.Molecule type: Protein
A.Residues: 21-73,'E','75-121,'PG','124-125,'E','127-139 <MAC>
A.Note: some carboxyl-terminal heterogeneity was found
C.Genetics:
A.Introns: 5/3; 61/3
C.Superfamily: pituitary glycoprotein hormone beta chain
C.Keywords: blocked amino end; glycoprotein; hormone; pituitary
F.1-20/Domian: signal sequence #status experimental <STG>
F.21-14/Product: lutropin beta #status experimental <LTB>
F.21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #s
F.29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F.33/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match          29.1%; Score 210; DB 1; Length 141;
Best Local Similarity 38.4%; Pred. No. 1.6e-13;
Matches 48; Conservative 21; Mismatches 46; Indels 10; Gaps 5;

OY    6 LFLGPALLLAGYCVGLASSGNLTFVGAVREFTLIARKPGCR-GLRTTTDACMGRC 64
       :| : | | : | : | | | | | | | | | | | | | | | | | | | | |
DB    3 MEQGLLLWLLGVAG--VMASGRPLRL--CGPIATILAARCKACRPVCITTTTSLCAGYC 58
       : : : | : | : | | | | | | : | : | | | | | | | | | | | |

OY    65 ETWEK--PILERPYTEAHNRCTYNETNKOTVTLPCNAAGVDPEFYTVPAIRCDCGACST 122
       : : : | : | : | | | | | | : | : | | | | | | | | | | | |

```

[illegible]

A:Accession: B60626
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-141 <CHN>
A:Note: parts of this sequence, including the amino and carboxyl ends of the mature p
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; hormone; pituitary
F:1-24/Domains: signal sequence #status predicted <Sig>
F:25-139/Product: gonadotropin beta chain #status experimental <Mat>
F:30-55,44-78,47-109,59-131,93-121,111-114/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 28.7% Score 207; DB 1; Length 141;
Best Local Similarity 42.5% Pred. No. 3,1e-13;
Matches 37; Conservative 16; Mismatches 32; Indels 2; Gaps 2;

OY 42 TFLAKKPGC-RGLRITTDACMGRCETWEKPILEPPYLEAHNRVCTYNETKQVTALPNCA 100
 | : | | : | | : | | : | | : | | : | | : | | : | | : |
DB 36 TVAVEKECCPRCKLVHQTTCISGHCLT-KEPYKSPSTFYGVHCVCYRDVRRETVRLDPCP 94
 | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 101 PGVDPEFTYTPVAIRCDGAGCATTEEC 127
 | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 95 PGVDPHITYPVALLSCDCSLCTMDTSDC 121
 | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
S16763
gonadotropin beta chain - grass carp
C:Species: Ctenopharyngodon idella (grass carp)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A:Accession: S16763
R:Chang, Y.S.; Huang, F.L.; Lo, T.B.
submitted to the EMBL Data Library, July 1991
A:Description: The cDNA cloning and primary structures of grass carp gonadotropin sub
A:Reference number: S16762
A:Accession: S16763
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-146 <CHN>
A:Cross-references: EMBL:X61051; NID:g62708; PIDN:CAA43385.1; PID:g62709
C:Superfamily: pituitary glycoprotein hormone beta chain
F:35-60,49-83,52-114,64-136,98-126,116-119/Disulfide bonds: #status predicted

Query Match 28.7% Score 207; DB 1; Length 146;
Best Local Similarity 42.5% Pred. No. 3.2e-13;
Matches 37; Conservative 16; Mismatches 32; Indels 2; Gaps 2;

OY 42 TFLAKKPGC-RGLRITTDACMGRCETWEKPILEPPYLEAHNRVCTYNETKQVTALPNCA 100
 | : | | : | | : | | : | | : | | : | | : | | : | | : |
DB 41 TVAVKECCPRCKLVHQTTCISGHCLT-KEPYKSPSTFYGVHCVCYRDVRRETVRLDPCP 99
 | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 101 PGVDPEFTYTPVAIRCDGAGCATTEEC 127
 | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 100 PGVDPHITYPVALLSCDCSLCTMDTSDC 126
 | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 5
UTSHB
lutropin beta chain precursor - sheep
N:Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; lutelinfz1
C:Species: Ovis orientalis aries, ovis ammon aries (domestic sheep)
C>Date: 24-Apr-1984 #sequence_revision 19-Jan-2001 #text_change 19-Jan-2001
C:Accession: I46949; S09232; A92110; A90053; B61096; A01500
R:Brown, P.; McNeilly, J.R.; Wallace, R.M.; McNeilly, A.S.; Clark, A.J.
Mol. Cell. Endocrinol. 93, 157-165, 1993
A>Title: Characterization of the ovine LH beta-subunit gene: the promoter directs gon
A:Reference number: I46949; MUID:93351742
A:Accession: I46949
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-141 <BRO>

A:Cross-references: GB:564695; NID:9408240; PIDN:AA827819.1; PID:9408241
 R.d'Angelo-Bernard, G.; Mounni, M.; Jutisz, M.; Counis, R.
 Nucleic Acids Res. 18, 2175, 1990
 A>Title: Cloning and sequence analysis of the cDNA for the precursor of the beta subunit
 A:Reference number: 509232; MUID:90245669
 A:Accession: 509232
 A:Molecule type: mRNA
 A:Residues: 1-58, 'L', '60-62, 'Q', '64-141 <ANG>
 A:Cross-references: EMBL:X52488; NID:91319; PIDN:CAA36729.1; PID:91320
 R.Liu, W.K.; Nahn, H.S.; Sweeney, C.M.; Holcomb, G.N.; Ward, D.N.
 J. Biol. Chem. 247, 4365-4381, 1972
 A>Title: The primary structure of ovine luteinizing hormone. II. The amino acid sequence
 A:Reference number: A92110; MUID:7221145
 A:Accession: A92110
 A:Molecule type: protein
 A:Residues: 21-121, 'PG', '124-125, 'E', '127-139 <LIU>
 R.Saizum, M.R.; Samy, T.S.A.; Papkoff, H.; Li, C.H.
 Arch. Biochem. Biophys. 153, 572-586, 1972
 A>Title: The primary structure of ovine interstitial cell-stimulating hormone. II. The b
 A:Reference number: A90053; MUID:73190035
 A:Accession: A90053
 A:Molecule type: protein
 A:Residues: 21-29, 'E', '31-71, 'P', '72-80, 'Q', '82-121, 'PG', '124-125, 'E', '127-139 <SA>
 R.Nomura, K.; Tsunasea, S.; Ohmura, K.; Sakiyama, F.; Shizume, K.
 Endocrinology 123, 700-712, 1988
 A>Title: Renotropic activity in ovine luteinizing hormone isoform(s).
 A:Reference number: A61098; MUID:88283534
 A:Accession: B61098
 A:Molecule type: protein
 A:Residues: 21-39, 'N', '41-49, '64-78, 'V', '80-82, '84-106, '115-121, 'PG', '124-138 <NO>
 A>Note: This form was designated form beta-3; forms beta-1 and beta-2 each lack several
 C:Genetics:
 A:Introns: 5/3; 61/3
 C:Superfamily: pituitary glycoprotein hormone beta chain
 C:Keywords: blocked amino end; glycoprotein; hormone; pituitary
 F:1-20/Domain: signal sequence #status predicted <IG>
 F:21-141/Product: luteotropin beta chain #status experimental <AT>
 F:21/Modified site: blocked amino end (Ser) (in mature form) (partial) (probably acetyla
 F:29-54, '43-77, '46-108, '58-130, '92-120, '110-113/disulfide bonds: #status predicted
 F:33/Binding site: carbohydrate (Asn) (covalent) #status experimental

```

Query Match          27.9%; Score 201.5; DB 2; Length 140;
Best Local Similarity 38.9%; Pred. No. 1.1e-12;
Matches 42; Conservative 16; Mismatches 47; Indels 3; Gaps 3;

Oy      21 CVLGASSGNLRTFVGCAREFTFLAKKPGC-RGLRITTDACMGRCETWKPILPEPYIEA 79
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      16 CHLVASAGG-SLLPCEPDINETFISEVKDCPKCLVFQSGISGHCHT-KDPSYKSPSLTV 73
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Oy      80 HHRCTVNETKQVYWKLPNCAPGVDPFTTYVAIRCDGACSTATTTC 127
       ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db      74 YQRVCTDYRVRETYRLDPDCRGVDPHVTFPVALSCDNLCTMDTSDC 121
       ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

RESULT 7
C36179
gonadotropin II beta chain precursor - chum salmon
C:Species: Oncorhynchus keta (chum salmon)
C:date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: C36179; S09344
R:Sekine, S.; Saito, A.; Itoh, H.; Kawachi, H.; Itoh, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 8645-8649, 1989
A>Title: Molecular cloning and sequence analysis of chum salmon gonadotropin cDNAs.
A:Reference number: A36179; MUID:90046849
A:Accession: C36179
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-142 <SEK>
A:Cross-references: GB:M27154; NID:g213429; PIDN:AAA49409.1; PID:g213430
R:Itou, H.; Suzuki, K.; Kawachi, H.
Gen. Comp. Endocrinol. 71, 438-451, 1988
A>Title: The complete amino acid sequences of beta-subunits of two distinct chum salm
A:Reference number: S07216; MUID:85053031
A:Accession: S09344
A:Molecule type: protein
A:Residues: 24-72, 'I', 74-142 <ITO>
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; heterodimer; hormone; pituitary
F:1-24/142/Product: gonadotropin II beta chain #status experimental <MAT>
F:29-54, 43-77, 46-108, 58-130, 92-120, 110-113/Disulfide bonds: #status predicted
F:33/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          27.8%; Score 201; DB 1; Length 142;
Best Local Similarity 34.7%; Pred. No. 1.2e-12;
Matches 42; Conservative 19; Mismatches 44; Indels 16; Gaps 3;

Oy      22 VIGASSGNLRTFVGCAVE-----PTFLAKKPGC-RGLRITTDACMGRET 66
       || | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      1 MGHLVGLISLFCLILEPVESLMQPQPIQNVLSLEKGCPCICLTIOPTISGHCVT 60
       || | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Oy      67 WEKPLPEPPYEIAHHRVCTVNETKOVTKLPNCAPGVDPFTTYVAIRCDGACSTATTE 126
       || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      61 KEPLFKSPFSIVYQHCTYRDVRETYRLDPDCRWDPHTTYVALSCDSCNLNMOTSD 119
       || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Oy      127 C 127
       |
Db      120 C 120

RESULT 8
I50554
gonadotropin II beta subunit - mummichog
C:Species: Fundulus heteroclitus (mummichog)
C:date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: I50554
R:Llin, T.W.; Ruppnow, B.A.; Price, D.A.; Greenberg, R.M.; Wallace, R.A.
Mol. Cell. Endocrinol. 85, 127-139, 1992
A>Title: Fundulus heteroclitus gonadotrops. 3. Cloning and sequencing of gonadotrop
A:Reference number: I50553; MUID:92405806
A:Accession: I50554
A>Status: preliminary; translated from GR/EMBL/DDB3
A:Molecule type: mRNA

```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 9, 2002, 13:34:05 ; Search time 11.87 Seconds
(without alignments)
424.056 Million cell updates/sec

Title: US-09-723-970-1
Perfect score: 722
Sequence: 1 MKLAFLEFLGPMALLLAGYG.....VAIRDCGACSTATTECETI 130

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	213.5	29.6	149	1	GTH2_CLUPA
2	210	29.1	141	1	LSHB_BOVIN
3	209	28.9	140	1	GTH2_CARAU
4	209	28.9	144	1	GTH2_CYPCA
5	207	28.7	141	1	GTH2_HYPMO
6	207	28.7	146	1	GTH2_CTEID
7	204	28.3	138	1	GTH2_CIAGA
8	202.5	28.0	141	1	LSHB_SHEEP
9	201.5	27.9	140	1	GTH2_ANGAN
10	201	27.6	142	1	GTH2_ONCKE
11	199	27.4	136	1	GTH2_FUNHE
12	198	27.3	113	1	GTHB_MORCI
13	197	27.3	115	1	GTH2_THUOB
14	196	27.1	107	1	FSHB_RANCA
15	192	26.6	142	1	GTH2_ONCMA
16	189	26.2	112	1	LSHB_RANCA
17	189	26.2	139	1	GTH2_MORSA
18	186.5	25.8	142	1	GTH2_CORAU
19	186.5	25.8	169	1	LSHB_EOUBU
20	184.5	25.6	169	1	LSHB_EOUBA
21	184	25.5	142	1	GTH2_ONCTS
22	184	25.5	146	1	GTH2_TRITC
23	183.5	25.4	169	1	LSHB_HORSE
24	181	25.1	137	1	GTH2_ACALA
25	180.5	25.0	141	1	LSHB_CERST
26	178	24.7	128	1	LSHB_PROSU
27	178	24.7	141	1	LSHB_RAT
28	176	24.4	141	1	LSHB_TRIVU
29	175	24.2	126	1	FSHB_PHOSU
30	175	24.2	141	1	LSHB_MOUSE
31	174	24.1	141	1	LSHB_PIG
32	173	24.0	138	1	LSHB_MACRU
33	172.5	23.9	138	1	LSHB_CANFA

34	171	23.7	147	1	FSHB_ANGAN	Q08127 anguilla an
35	167	23.1	129	1	FSHB_CAVPO	Q91K69 cavia porce
36	165	22.9	118	1	LSHB_BALAC	P33088 balaenopter
37	164	22.7	128	1	LSHB_STRCA	P80664 struthio ca
38	164	22.7	129	1	FSHB_HUMAN	P01225 homo sapien
39	164	22.7	129	1	FSHB_TRIVU	Q46430 trichosurus
40	164	22.7	130	1	FSHB_MOUSE	Q06087 mus musculu
41	163.5	22.6	143	1	LSHB_FELCA	Q77805 felis silve
42	163	22.6	130	1	FSHB_RAT	P18427 rattus norv
43	162	22.4	129	1	FSHB_PIG	P01228 sus scrofa
44	162	22.4	141	1	LSHB_HUMAN	P01229 homo sapien
45	161	22.3	118	1	LSHB_PHYCA	P25330 physeter ca

ALIGNMENTS

RESULT 1
ID GTH2_CLUPA STANDARD; PRT; 149 AA.
AC 09YGH2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Gonadotropin beta-II chain precursor (GTH-II-beta).
OS Clupea pallasii (Pacific herring).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
OC Clupeinae; Clupea.
OX NCBI_TaxID=30724;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Plutitary;
RA Power M.E., Carolisfield J., Wallis G.P., Sherwood N.M.:
RT Isolation and characterization of a cDNA for gonadotropin II-beta of
RT Pacific herring, an ancient teleost.";
RL J. Fish Biol. 50:315-323(1997).
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
FAMILY.
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X91984; CAA63038.1; -
DR HSSP; P01233; 1XU.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Glyco_hormone_beta.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 1 149
FT 149 GONADOTROPIN BETA-II CHAIN.
FT DISULFID 30 78 BY SIMILARITY.
FT DISULFID 44 93 BY SIMILARITY.
FT DISULFID 47 131 BY SIMILARITY.
FT DISULFID 55 109 BY SIMILARITY.
FT DISULFID 59 111 BY SIMILARITY.
FT DISULFID 121 121 BY SIMILARITY.
FT CARBOHYD 34 34 N-LINKED (GLCNAC...) (POTENTIAL).
SO SEQUENCE 149 AA; 16627 MW; 4585DCB34367069 CRC64;

Query Match 29.6%; Score 213.5; DB 1; Length 149;
Best Local Similarity 38.8%; Pred. No. 3.2e-15;

```

Matches 47; Conservative 18; Mismatches 49; Indels 7; Gaps 4;
QY      10 PRAALLLLAGYGCVLG--ASSGNLRFVYCAGAAEFETFLAKKPGC-RGLRITTDACGRCEI 66
       1 :||| |||| | ||: | : | : ||| ||| | : ||| |
Db       5 PECTILLILCMCKVLAVPACCENLPD---CVLVNETVSYVERECGPRCLVFRTTIGSGHCPT 61
QY      67 WEKPILEPPYEIAHNRVCVTYNMETKNQVTKLPLPCACAGVPPEFYYPPAIRIDCGACSTATTE 126
       ::| : | : ||| : :||::|| ||| ||||| :||| || :| :
Db      62 -KEPYKKSPFSFVNQHVCYTGNFRRETIRLPDCACAGVDPLYTYYPALSSCCSLCSMDISD 120
OY      127 C 127
       |
Db      121 C 121

RESULT 2
LSHB_BOVIN STANDARD; PRT; 141 AA.
ID LSHB_BOVIN
AC P04651;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-beta) (LSH-B) (LH-B).
GN LHB.
OS Bos taurus (bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
CX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85207729; PubMed=2987241;
RA Virgin J.B., Silver B.J., Thomson A.R., Nilsson J.H.;
RT "The gene for the beta subunit of bovine luteinizing hormone encodes a gonadotropin mRNA with an unusually short 5'-untranslated region.";
RL J. Biol. Chem. 260:7072-7077(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85182575; PubMed=3838746;
RA Maurer R.A.;
RT "Analysis of several bovine lutropin beta subunit cDNAs reveals heterogeneity in nucleotide sequence.";
RL J. Biol. Chem. 260:4684-4687(1985).
RN [3]
RP SEQUENCE OF 21-1139.
RX MEDLINE=74075724; PubMed=4770795;
RA Maguinn-Rogister G., Hennen G.;
RT "Luteinizing hormone. The primary structures of the beta-subunit from bovine and porcine species.";
RL Eur. J. Biochem. 39:235-253(1973).
CC -!- EDUCATION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTOPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HOMONES BETA CHAIN FAMILY.
-----
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CC
DR EMBL; M10077; AAA30623.1; -.
DR EMBL; M11506; AAB59267.1; -.
DR PIR; A01499; UTBOB.
DR HSSP; P01233; 1XUL.
DR GlycoSuiteDB; P04651; -.
DR InterPro; IPR000359; Cys_knot.
```

[illegible]

[illegible]

```
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENSIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN FAMILY.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or\_send\_an\_email\_to\_license@isb-sib.ch).
CC -----
CC DR EMBL; X61051; CAA4385.1; -.
CC DR PIR; S16763; S16763.
CC DR HSSP; P01233; IXUL.
CC DR InterPro: IPR000359; Cys_knot.
CC DR InterPro: IPR001545; Glyco_hormone_beta.
CC DR Pfam; PF00007; Cys_knot; 1.
CC DR SMART; SM00068; GHB; 1.
CC DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
CC DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
CC KW Hormone; Glycoprotein; Signal.
CC FT NON_TER 1
CC FT SIGNAL 2
CC FT CHAIN 29 146 BY SIMILARITY.
CC FT DISULFID 35 83 GONADOTROPIN BETA-II CHAIN.
CC FT DISULFID 49 98 BY SIMILARITY.
CC FT DISULFID 52 136 BY SIMILARITY.
CC FT DISULFID 60 114 BY SIMILARITY.
CC FT DISULFID 64 116 BY SIMILARITY.
CC FT DISULFID 119 126 BY SIMILARITY.
CC FT CARBOHYD 39 39 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 146 AA; 16320 MW; 69173444C679082 CRC64;
CC -----
QY Query Match 28.7%; Score 207; DB 1; Length 146;
Db Best Local Similarity 42.5%; Pred. No. 1.5e-14;
Matches 37; Conservative 16; Mismatches 32; Indels 2; Gaps 2;
QY 42 TFLAKRPGC-RGLRTITDACWGRCETWEKRPILLEPPYLEAHNRCTYNFTKQVTKLPNCA 100
   1 : : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 41 TVAVEKEGCPKCLVPOQTICSHCLLT-KEPYKKSPSTFYGVCTCYRVRYRETVRLPCDP 99
QY 101 PGVDPFYTPVAIKRCDCGACSTATIEEC 127
   1 | | | | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
Db 100 PGVDPFITYPVALLSCDCSLCTMDTSDC 126
-----
RESULT 7
PTH2_CLAGA STANDARD: PRT: 138 AA.
AC P53543;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gonadotropin beta-II chain precursor (PTH-II-beta).
OS Clarias gariepinus (Sharptooth catfish) (African catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Siluriformes; Clariidae; Clarias.
OC NCBI_TaxID=13013;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Pituitary;
RA Reuters F.E.W., Jensen C.P., Schultz R.W., Goos H.J.T., Bogerd J.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 22-138.
RC TISSUE-Pituitary;
RX MEDLINE=93051153; PubMed=1426937;
RA Koide Y., Noso T., Schouten G., Peute J., Zandbergen M.A., Bogerd J.,
Schultz R.W., Kawachi H., Goos H.J.;
```


FT	DISULFID	54	108		BY SIMILARITY.					
FT	DISULFID	58	110		BY SIMILARITY.					
FT	DISULFID	113	120							
FT	MOD_RES	21	21		BLOCKED.					
FT	CARBOND	33	33		N-LINKED (GLCNAC. . .).					
FT					-FTID-CAR_000046.					
FT	VARIANT	138	141		MISSING (IN SOME MOLECULES).					
FT	CONFLICT	30	30		Q -> E (IN REF. 4).					
FT	CONFLICT	59	59		L -> P (IN REF. 1).					
FT	CONFLICT	63	63		R -> Q (IN REF. 2).					
FT	CONFLICT	71	72		PM -> PPM (IN REF. 4).					
FT	CONFLICT	81	81		E -> Q (IN REF. 4).					
FT	CONFLICT	122	123		GP -> PG (IN REF. 3 AND 4).					
FT	CONFLICT	126	126		Q -> E (IN REF. 3 AND 4).					
SO	SEQUENCE	141 AA;	15184 MW;		C59EC7C0AA55A9DC CRC64;					
Query Match		28.0%;	Score 202.5;	DB 1;	Length 141;					
Best Local Similarity		39.2%;	Pred. No. 4.1e-14;							
Matches 47;		Conservative 19;	Mismatches 45;	Indels 9;	Gaps 5;					
Oy	11 MALLLLAGCVGLGASSGNLTFTVCGAAYREFFLAKPGCR-GLRTITPDACGRCEYWK 69									
Db	7 LLLMILLGVAGV-WASRGRLRL--CQPLNATLAAEKKACPCITFTTICAGYCLSKMR 63									
Oy	70 --PILEPYIEAHNRCTYNETKQVTKLPCNAGVDPYPTVPAVIRCDGACSTATTEC 127									
Db	64 VLPVILPMPQ---RVCFTHELRFAVSRLPGCPGVDPMVSPVALSCHGCRSLSTDC 120									
RESULT 9										
ID	GTH2_ANGAN		STANDARD:	PRT:	140 AA.					
AC	P27767;									
DT	01-AUG-1992 (Rel. 23, Created)									
DT	01-AUG-1992 (Rel. 23, Last sequence update)									
DT	16-OCT-2001 (Rel. 40, Last annotation update)									
DE	Gonadotropin beta-II chain precursor (GTH-II-beta).									
OS	Anguilla anguilla (European freshwater eel).									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
OC	Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;									
OC	Anguillidae; Anguilla.									
OX	NCBI_TaxID=7936;									
RN	[1]									
RE	SEQUENCE FROM N.A.									
RC	TISSUE=Pituitary;									
RX	MEDLINE=90334705; PubMed=2116136;									
RA	Quezat B., Mounni M., Jutisz M., Fontaine Y.A., Counis R.;									
RT	"Molecular cloning and sequence analysis of the cDNA for the putative									
RT	beta subunit of the type-II gonadotropin from the European eel.";									
RL	J. Mol. Endocrinol. 4:257-264(1990).									
CC	-I- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.									
CC	-I- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.									
CC	-I- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN									
CC	FAMILY.									
CC	-----									
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ ,									
CC	or send an email to license@sib-sib.ch).									
CC	-----									
DR	EMBL: X61039; CAA43374.1; -.									
DR	PIR: A48166; A48166.									
DR	HSSP: P01233; 1XUL.									

[illegible]

DR InterPro: IPR001545; Glyco_hormone_beta.
DR Pfam: PF00007; Cys_knot; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR SMART: SM00068; GHb: 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
DR Hormone; Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 29 142 GONADOTROPIN BETA-II CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .).
FT VARIANT 73 73 Y -> I.
FT VARIANT 86 86 T -> K.
SQ SEQUENCE 142 AA; 15872 MW; E31E117DA235C486 CRC64;

Query Match 27.8%; Score 201; DB 1; Length 142;
Best Local Similarity 34.7%; Pred. No. 5.9e-14;
Matches 42; Conservative 19; Mismatches 44; Indels 16; Gaps 3;

QY 22 VLGASSGNLFREFGCAVE-----FTFLAKKPGC-RGLRITTDACMGRCET 66
Db 1 MLGHLVGLILFLCILEPVEGSLMPCOPINOTVSLKSGCPTCLVITPTICSGHCVT 60

QY 67 WEKPILEPPYIAHHRCVYNETKQVTKLPNCAGVDPFYTPVAIRCDGACSTATTE 126
Db 61 -KEPVFSFSTVYOHCTYRDVRETRILPDCPPWDPHTYTPVALSCDCLCMNDTSD 119

QY 127 C 127
Db 120 C 120

RESULT 11
GTHB_FUNHE STANDARD; PRT; 136 AA.
AC P30972;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gonadotropin beta-II chain precursor (GTH-II-beta).
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OX NCBI_Taxid=8078;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=92405806; PubMed=1526312;
RA Lin Y.-W.P., Runow B.A., Price D.A., Greenberg R.M., Wallace R.A.;
RT "Fundulus heteroclitus gonadotropins. 3. Cloning and sequencing of
gonadotropic hormone (GTH) I and II beta-subunits using the
polymerase chain reaction.";
RL Mol. Cell. Endocrinol. 85:127-139(1992).
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
FAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL: M87015; AAB59963.1; -
DR HSSP: P01233; IXUL.
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR001545; Glyco_hormone_beta.
DR Pfam: PF00007; Cys_knot; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR SMART: SM00068; GHb: 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
DR Hormone; Hormone; Glycoprotein.
FT SIGNAL 1 21
FT CHAIN 22 136 GONADOTROPIN BETA-II CHAIN.
FT DISULFID 27 75 BY SIMILARITY.
FT DISULFID 41 90 BY SIMILARITY.
FT DISULFID 44 128 BY SIMILARITY.
FT DISULFID 52 106 BY SIMILARITY.
FT DISULFID 56 108 BY SIMILARITY.
FT DISULFID 111 118 BY SIMILARITY.
FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 136 AA; 15016 MW; 716576844A6A1653 CRC64;

Query Match 27.6%; Score 199; DB 1; Length 136;
Best Local Similarity 41.9%; Pred. No. 9.1e-14;
Matches 39; Conservative 12; Mismatches 40; Indels 2; Gaps 2;

QY 36 CAVEEFFLAKKPGCRGL-RITTDACMGRCETWEKPILEPPYIAHHRCVYNETKQV 94
Db 27 COLNLQNTLSLEKRCGSGCHRVETITSGCAT-KDPNFKTSYKNAIGHVCTGYGLDYKTF 85

QY 95 KLPNCAGVDPFYTPVAIRCDGACSTATTEC 127
Db 86 EFPVCVPGVDPVTPVPAALSCGCGCAMATSDC 118

RESULT 12
GTHB_MURCI STANDARD; PRT; 113 AA.
AC P12837;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Gonadotropin beta chain.
OS Muranesox cinereus (Pike eel) (Daggeetooth pike conger).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Congridae;
OC Muranesocidae; Muranesox.
OX NCBI_Taxid=7946;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=90092087; PubMed=2598923;
RA Liu C.-S., Huang F.-L., Chang Y.-S., Lo T.-B.;
RT "Pike eel (Muranesox cinereus) gonadotropin. Amino acid sequences of
both alpha and beta subunits.";
RL Eur. J. Biochem. 186:105-114(1989).
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
FAMILY.

CC PIR: S07092; S07092.
DR HSSP: P01233; IXUL.
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR001545; Glyco_hormone_beta.
DR Pfam: PF00007; Cys_knot; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR SMART: SM00068; GHb: 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Glycoprotein.

Search completed: July 9, 2002, 13:37:35.
Job time: 210 sec

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AC P48253;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gonadotropin beta-II chain precursor (GTH-II-beta).
OS Oncorhynchus masou (Cherry salmon) (Masu salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8020;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=94197893; Pubmed=8148035;
RA Kato Y., Gen K., Maruyama O., Tomizawa K., Kato T.;
RT "Molecular cloning of cDNAs encoding two gonadotrophin beta subunits
RT (GTH-I beta and -II beta) from the masu salmon, Oncorhynchus masou:
RT rapid divergence of the GTH-I beta gene."
RL J. Mol. Endocrinol. 11:275-282(1993).
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: S69276; AAB30424.1; -.
DR HSSP: P01233; 1XUL.
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR001545; Glyco_hormone_beta.
DR Pfam: PF00007; Cys_knot; 1.
DR PRINTS: PRO0438; GFCYSKNOT.
DR SMART: SM00068; GHB; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Glycoprotein; Signal.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 142 GONADOTROPIN BETA-II CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 142 AA; 15684 MM; 70A3906EAEAB3FFF CRC64;

Query Match 26.6%; Score 192; DB 1; Length 142;
Best Local Similarity 33.9%; Pred. No. 5e-13;
Matches 41; Conservative 18; Mismatches 46; Indels 16; Gaps 3;

QY 22 VLASSGNLRTFVCGAVRE-----FTFLAKKPGC-RGLRITTDACWGRCE 66
DB 1 MGLGHVGLISLCLILEPEVGSIMOPCOPINQTVSLEKGCPTCLVITPTICSGHCIT 60
QY 67 WEKPLLEPPYLEAHHRYCTVNETKOVYKLPNCAPGVDPFTYPAVIRCDGACSTATTE 126
DB 61 -KEPVFRSPFSTVYQHCTYDRVIREMIRLPDCPPWVDPHVYTPVALSCDCSLCNDTSD 119
QY 127 C 127
DB 120 C 120
```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 9, 2002, 13:33:25 ; Search time 27.1 Seconds
(without alignments)
829.865 Million cell updates/sec

Title: US-09-723-970-1
Perfect score: 722
Sequence: 1 MKIAFLGLPMALLLAGYG.....VAIRDCGACSTATTECETI 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_podent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_rvirus:*
17: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	211	29.2	128	13	091997
2	208	28.8	140	13	098173
3	205.5	28.5	123	13	0902K1
4	204.5	28.3	142	13	090D92
5	201.5	27.9	137	13	090WC1
6	201	27.8	140	13	090D80
7	195	27.0	145	13	090W55
8	194.5	26.9	146	13	090W19
9	192.5	26.7	131	13	090W63
10	191.5	26.5	145	13	090WD2
11	189	26.2	137	13	091999
12	189	26.0	146	13	090DEH0
13	188	26.0	138	13	090WC9
14	186.5	25.8	88	13	090W07
15	180	24.9	135	11	0924A7
16	180	24.9	141	11	0924A8

17	179	24.8	121	13	090W64	090W64 scyllorhinu
18	178	24.7	139	11	062778	062778 rattus norv
19	175	24.2	127	11	0924A6	0924A6 cavia porce
20	174	24.1	165	6	09BEH2	09BEH2 macaca fasc
21	173.5	24.0	142	6	09BD19	09BD19 panthera tl
22	168.5	23.3	132	13	090D81	090D81 ictalurus p
23	167.5	23.2	141	6	095J85	095J85 monodelphis
24	165	22.9	129	6	095J82	095J82 monodelphis
25	164	22.7	165	6	09BEH1	09BEH1 macaca fasc
26	161	22.3	129	6	09BD10	09BD10 panthera tl
27	160	22.2	150	13	013051	013051 cyprinus ca
28	159	22.0	147	13	013052	013052 ctenopharyn
29	159	22.0	150	13	09PW21	09PW21 aristichthy
30	158	21.9	125	13	091992	091992 conger cong
31	157	21.7	109	13	091998	091998 acipenser b
32	154.5	21.4	138	4	016163	016163 homo sapien
33	154	21.3	89	6	046618	046618 equus zebra
34	154	21.3	89	6	046619	046619 equus hemio
35	149.5	20.7	82	6	046622	046622 ceratotheri
36	149	20.6	123	13	09W608	09W608 salmo salar
37	148	20.5	130	13	098172	098172 myliopharyng
38	145	20.1	165	6	09GL37	09GL37 macaca mula
39	145	20.1	165	11	099P48	099P48 mus musculu
40	144	19.9	138	6	095J88	095J88 monodelphis
41	144	19.9	149	13	09PW9	09PW9 carassius a
42	144	19.9	150	13	013049	013049 carassius a
43	143.5	19.9	137	13	090D93	090D93 oncorhynch
44	137.5	19.0	80	11	063013	063013 rattus norv
45	134.5	18.6	130	13	0911B3	0911B3 carassius a

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	128 AA.
091997	091997	091997		
AC	091997	091997		
DT	01-OCT-2000 (TREMBLER, 15, Created)			
DT	01-OCT-2000 (TREMBLER, 15, Last sequence update)			
DT	01-DEC-2001 (TREMBLER, 19, Last annotation update)			
DE	FOLLICLE-STIMULATING HORMONE PRECURSOR.			
GN	FSH.			
OS	Acipenser baerii (Siberian sturgeon).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;			
OC	Acipenserinae; Acipenser.			
OX	NCBI_TaxID=27689;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PITUITARY;			
RX	MEDLINE=20318422; PubMed=10859263;			
RA	Querat B., Sellouk A., Salmon C.;			
RT	*Phylogenetic analysis of the vertebrate glycoprotein hormone family including new sequences of sturgeon (Acipenser baerii) subunits of the two gonadotropins and the thyroid stimulating hormone.*;			
RT	two gonadotropins and the thyroid stimulating hormone.*;			
RL	Biol. Reprod. 63:222-228(2000).			
DR	EMBL; AJ251658; CAB93504.1; -.			
DR	HSSP; P01233; IYUL.			
DR	InterPro; IPR000359; Cys_knot.			
DR	InterPro; IPR001545; Glyco_hormone_beta.			
DR	Pfam; PF000007; Cys_knot; 1.			
DR	SMART; SM00068; GHB; 1.			
DR	PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.			
KW	Signal.			
FT	SIGNAL			
FT	CHAIN			
FT	SEQUENCE			

Query Match 29.28; Score 211; DB 13; Length 128;
Best Local Similarity 42.7%; Pred. No. 1,7e-16;
Matches 41; Conservative 15; Mismatches 38; Indels 2; Gaps 2;

OY		36	CAYRETFELFAKPGRG- CALLENTITIGEDGCGNCVSVNFTSCAGRCGLT-QADVIYKSISLYTLQWCTKEI SYTYIV	94
Dd		22	CALENTITIGEDGCGNCVSVNFTSCAGRCGLT-QADVIYKSISLYTLQWCTKEI SYTYIV	80
Oy		95	KLPNCAPGVDFPYTPVAIRCDGCAGSTATTECEPI 130	
Dd		81	QLPNCPEHVDPFYTPVALSCGCAFDYTDCGLT 116	
RESULT		2		
O98TV3	ID	PRELIMINARY;	PRT; 140 AA.	
O98TV3	AC	O98TV3;		
DT		01-JUN-2001 (TREMBLrel. 17, last sequence update)		
DT		01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE		LUTEINIZING HORMONE BETA SUBUNIT.		
OS		Mylolpharyngodon plicus.		
OC		Eukaryaota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprindidae; Mylolpharyngodon.		
OX		NGBL_TaxID=735356;		
RN	[1]	SEQUENCE FROM N.A.		
RA	Bayer-Eitzenberg D., Rosenfeld H., Zmora N., Yaron Z., Elizur A.;			
RL	"Isolation and characterization of the black carp LH beta subunit."			
DR	Submitted (NOV-2000) to the EMBL/Genbank/DDBJ databases.			
EMBL:	AF319960; AAA07414.1; -.			
HSSP:	P01233; IXL.			
InterPro:	IPR000359; Cys_knot.			
IntraPro:	IPR001545; Glyco_hormone_beta.			
SFAM:	PF00007; Cys_knot; 1.			
SMART:	SM00068; GHB; 1.			
PROSITE:	PS00261; GLYC_HORMONE_BETA_1; UNKNOMN_1.			
PRSITE:	PS00689; GLYC_HORMONE_BETA_2; 1.			
SQ	SEQUENCE 140 AA; 15820 MW; 8Fi27Z3FF35D5A010 CRC64;			
Query Match		28.8%; Score 208; DB 13; Length 140;		
Best Local Similarity		37.9%; Pred.No.4e-16;		
Matches 44; Conservative 19; Mismatches 49; Indels 4; Gaps				
OY		13 LLLLGVCVLDAASSGNLTFRFGCAVREFETFLAKPKGC-RGLRIITTDACMGRETWEKPT 71		
Dd		8 LLLLFVVYLILFAQSST--LRPCRVNETVAVERKGCCPLVFOTISSGHCLT-KEVY 64		
OY		72 LEPPYEAHNRVCYNIEIKOVTKLVPCNAVGDPFYTPVAIRCDCGAGATATEEC 127		
Dd		65 YKSPFEVTYGQHCTRYDRVHYETVRLEPDGPCPVGDPHITYPALSCDSLCTMTSDC 120		
RESULT		3		
O90ZK1	ID	PRELIMINARY;	PRT; 123 AA.	
O90ZK1	AC	O90ZK1;		
DT		01-DEC-2001 (TREMBLrel. 19, Created)		
DT		01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DE		FOLLICILE STIMULATING HORMONE BETA SUBUNIT PRECURSOR (FRAGMENT).		
OS		Rana ridibunda (Laughing frog) (Marsh frog).		
OC		Eukaryaota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.		
OX		NGBL_TaxID=8406;		
RN	[1]	SEQUENCE FROM N.A.		
RP	TISSUE=PITUITARY;			
RA	Querat B.;			
RT	"Evolution of glycoprotein hormones in gnathostomes.";			
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.			
EMBL:	AJ311356; CAC39253.1; -.			
Signal.				

FT	NON TER	1	1	POTENTIAL.
FT	SIGNAL	<1	16	FOLICLE STIMULATING HORMONE BETA
FT	CHAIN	17	123	SUBUNIT.
FT	SEQUENCE	123 AA;	13678 MW;	926C3E72EECCA85 CRC64;
Query Match		28.5%;	Score 205.5;	DB 13; Length 123;
Best Local Similarity		40.5%;	Pred. No. 6,8e-16;	
Matches		45;	Conservative	15; Mismatches 44; Indels 7; Gaps 4;
OY	19 YGVVLGASSGNLRTFVGCAVREFFFLAKKPGCGRLRITTDACW--GCETWEKPILLEPPY	76		
	: : : : : : : : : :			
DB	3 YGLVT---FMVMMLSATGEISNITIVLEKEEC-GACISVNATMGCGCYTMDPNLMYPQK	58		
OY	77 IEAHNRVCYNNTKQOVTKLRPNCAGVDPEFYTPPAIRCDGACSTATEC	127		
DB	59 SE-KQGVCTHYEVITYETVKIPGCCADNNPFYPAVADCHGCRNSSETIDC	108		
RESULT	4			
ID	Q9DG92	PRELIMINARY;	PRT:	142 AA.
AC	Q9DG92;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DR	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DI	LUTERINIZING HORMONE BETA SUBUNIT.			
GN	IH BETA.			
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;			
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.			
OX	NCBI_TaxID=8022;			
RN	[1]			
RP	SEQUENCE FROM N.A..			
RA	Morita T., Yoshizaki G., Takeuchi T.:			
RT	"rainbow trout lutelizing hormone beta subunit mRNA."			
RL	submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; AB050836; BABI7687.1; -			
DR	HSSP; P01233; 1XU.			
DR	InterPro: IPR000359; Cys_knot.			
DR	InterPro: IPR01545; Glyco_hormone_beta.			
DR	Pfam: PF00007; Cys_knot; 1.			
DR	SMART; SM00068; GHb; 1.			
DR	PROSITE; PS00261; GLYC_HORMONE_BETA_1; UNKNOWN_1.			
SO	SEQUENCE 142 AA; 15824 MW; 7c399c4fb1fae55a CRC64;			
Query Match		28.3%;	Score 204.5;	DB 13; Length 142;
Best Local Similarity		37.1%;	Pred. No. 1e-15;	
Matches		46;	Conservative	20; Mismatches 49; Indels 9; Gaps 5;
OY	6 LPLGPALLLLAGYCV-LGASSGNLRTFVGCAVREFFFLAKKPGC-RGLRITTDACMGR	63		
	: : : : : : : : : : : :			
DB	4 LVHGVLISILL-----CIILEPYEGSL-QPCQPINQIYSVEKCGPTCLVQTPICSGH	57		
OY	64 CETWEKPILLEPPYIEAHHNRVCYNNTKQOVTKLRPNCAGVDPEFYTPPAIRCDGACST	123		
	: : : : :			
DB	58 CVT-KEPVKSPFSFYQGAVCTRDVRETIRLPDPCRPVNDHVHTYPAVALSCDCSICNMND	116		
OY	124 TTFC 127			
	: :			
DB	117 TSDC 120			
RESULT	5			
ID	Q9OWC1	PRELIMINARY;	PRT:	137 AA.
AC	Q9OWC1;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DI	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			

QY 69 KPILEPIEIAHHHVCYNENETKOVTALEPNCAVDFPVTVPVAIRICDCGACSTATTEC 127
 :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 Db 62 EPVYKSFSFNINYGVCYTRDVRRETVFALPDRCRPGVDENVHYTPVALSCBCTICTMTDTSDC 120

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RESULT      7
O90W55 ID O90W55 PRELIMINARY; PRT; 145 AA.
OC AC O90W55:
DT DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE GNADOTROPIN (GTH-II) BETA SUBUNIT.
GN GTH-II BETA.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acantlopterygii; Percomorpha; Pleuronectiformes;
CC Pleuronectoidae; Paralicthyidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PITUITARY;
RX MEDLINE=21216564; Pubmed=11316417;
RA Kajimura S., Yoshiura Y., Suzuki M., Aida K.;
RT "cDNA cloning of two gonadotropin beta subunits (GTH-Ibeta and -IIbeta) and their expression profiles during gametogenesis in the Japanese flounder (Paralicthys olivaceus)."; Gen. Comp. Endocrinol. 122:117-129(2001).
RL EMBL; AB042423; BAB47388.1; -.
DR DR SEQUENCE 145 AA; 16295 MW; 8DDCE52EB3E750CC CRC64;


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Query Match 27.0%; Score 195; DB 13; Length 145;
Best Local Similarity 38.7%; Pred. No. 1.3e-14;
Matches 36; Conservative 18; Mismatches 37; Indels 2; Gaps 2;

QY 36 CAVAEFFFLAKRKPC-RGLRTTDPACMGCRCTMEKPILPEPIEAHHHCYNENETKVTV 94
Db 36 CLLNQIVSLERKECPCHVEFTTGSGHCKT-KDPAKIPPLMYOHCVTYQLYYKF 94
 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 95 KLPPNCGVDFPVFPVAIRCDCGACSTATTEC 127
 ||:|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 95 ELRPCPGVDPTVSYPVAVSCTCGCALNTSDC 127
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RESULT 8
O90W19 ID O90W19 PRELIMINARY; PRT; 146 AA.
OC AC O90W19:
DT DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE LH-BETA PROTEIN PRECURSOR.
GN LH-BETA.
OS Hippoglossus hippoglossus (Atlantic halibut).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acantlopterygii; Percomorpha; Pleuronectiformes;
CC Pleuronectoidae; Pleuronectidae; Hippoglossus.
OX NCBI_TaxID=8267;
RN [1]
RP SEQUENCE FROM N.A.
RC Weisslen F.A., Kobayashi T., Andersson E., Norberg B., Andersen O.;
RX "Molecular characterization of FSH-beta, LH-beta, and alpha-subunit of Atlantic halibut (Hippoglossus hippoglossus)."; Submitted (OCT-2001) to the EMBL/GeneBank/DDBJ databases.
RL EMBL; AJ417769; CAD10502.1; -.
DR KM Signal.
FM FT CHAIN 1 31
 FT CHAIN 32 146 LH-BETA SUBUNIT.
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	Query Match	26.2%	Score 189;	DB 13	length 146;
	Best Local Similarity	39.8%	Pred. No. 6	3e-14;	
	Matches	37;	Conservative	15;	Mismatches 37;
				Indels	4;
				Gaps	3
QY	36	CAVREFTFLAKKPCGGRGLR-TTDDACWGRCELEWEPDLEPPIEAEHHRCTYNETKQTV	94		
		: : : : : : : : : : : : : : :			
DB	39	COLINQVTSLEEGGCKPCHPVETTCGSCGCTI-KDPMKTRVYGH--VCYTRDLHYKTF	95		
QY	95	KLPNCAGVDPPEYTYVPAIRCDGAGCATTEEC	127		
		: : : : : : : : : : : : : : :			
DB	96	ELPDGCPGVDPVTYVPAVNSCHGCGCAMDTSDC	128		

	Query Match	26.0%	Score 188;	DB 13;	length 138;
	Best Local Similarity	35.3%;	Pred. No.7.8e-14;		
	Matches 41;	Conservative 16;	Mismatches 49;	Indels 10;	Gaps 3.
OY	13 LLLAGGYCIVLGASSGNRTFYGCACAVREFTFLAKKPGCR-GIRITTTDAGWGRCETWEKPI	71			
			:		: :

RESULT	14
Q9W6C7	
ID	Q9W6C7
AC	Q9W6C7;
DT	01-NOV-1999 (TrEMBLrel. 12, Created)
DT	01-NOV-1999 (TrEMBLrel. 12, last sequence update)
DI	01-JUN-2001 (TrEMBLrel. 17, last annotation update)
DE	GONADOTROPIN II BETA SUBUNIT (FRAGMENT).
OS	Salmo salar (Atlantic salmon);
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Achtiopterygii; Neopterygii; Teleostei; Euteleostei;
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX	NCBI_TaxID=8030;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=PITUITARY;
RA	yadette F., Goksorr A., Male R.;
RT	"Modulation of pituitary gonadotropin mRNA levels in juvenile Atlantic
RL	salmou by 4-nonylphenol.";
DR	Submitted (APR-1999) to the EMBL/Genbank/DDBJ databases.
DR	EMBL: AF146151; AAD34593.1; -
DR	HSSP: P01233; 1XUL.
DR	InterPro: IPR000359; Cys_knot.
DR	InterPro: IPR002400; GF_cysknot.
DR	InterPro: IPR001545; Glyco_hormone_beta.
DR	Pfam: PF00007; Cys_knot; 1.
DR	PRINTS: PRO0438; GECSKNKT.
DR	SMART: SMO0068; GHB; 1.
DR	PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR	PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
FT	NON_TER 1 88
FT	NON_TER 1 88
SQ	SEQUENCE 88 AA; 9975 MW; A6E9CB651E1A5536 CRC64;

Query Match	25.8%	Score 186.5	DB 13	Length 88
Best Local Similarity	41.2%	Pred. No. 7.2e-14		
Matches	33	Conservative 15	Mismatches 29	Indels 3
				Gaps 2
QY 48	PGCRRLRTTTPACMRCRCEIWEKPILEPPYIEAHNHVCYTNENKQYTVKILPNCAPGVDPFY	107		
Db 2	PTC--LVYQTFICSHCVT-KEPYKSPSFYVQYHVCYRDVRYETIRLPDRCPPVDHNV	58		
QY 108	TYPAVIRCDGACGACSTATTEC	127		
Db 59	TYPAVASCDCSLCNDMTSDC	78		

RESULT	15
0924A7	
ID	0924A7
AC	PRELIMINARY;
PRT:	135 AA.
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	LUTEINIZING HORMONE BETA SUBUNIT PRECURSOR (FRAGMENT).
OS	Cavia porcellus (Guinea pig).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
CC	Mammalia; Eutheria; Rodentia; Hystericognathii; Caviidae; Cavia.
OX	NCBI_TaxId=10141;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE#021255925; PubMed=11357063;
RA	Sherman G.B., Hellman D.F., Hoss A.J., Bunick D., Lund L.A.;
RT	"Messenger RNAs encoding the beta subunits of guinea pig (Cavia porcellus) luteinizing hormone (gplH) and putative chorionic

RT gonadotropin (gpcg) are transcribed from a single-copy gpLH/CSbeta
RT gene.¹
RL J. Mol. Endocrinol. 26:267-280(2001).
DR EMBL; AF356595; AAK84306.1; -.

RT gene."

RL J. Mol. Endocrinol., 26:267-280(2001).

DR EMBL; AF356595; AAK84306.1; -.

KW	Signal
FT	NON TE

FT	SIGNAL	1
11	MON_1 EN	1

FT CHAIN

LUTEINIZING HORMONE BETA SUBUNIT.

SQ SEQUENC

; A44C63DBDC5607AE CRC64;

SQ SEQUENC

Query Match

24.98; Score 180; DB 11; Length 135;

Best Local Similarity 35.4%; Pred. NO. 6.3e-13;
 Watcher 45; Concomitant 10; Mismatch 41

malchies	40;	conservative	19;	mischalchies	41;	lindels	24;	gaps	77;
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QY      6 LFLGPALLLLAGYGCVCAGSSGNLRTFVGCAVREFFLAKPCCR-GLRITTTACMGRC 64
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 LLLG-----LLLSFG--VWASRGRLRPY--CRPINATLAERKACPICTFTTSSICAGYC 52

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Db 1 LLLG----LLSTSG--VWASRGPLRPY--CRPINATLAEKEACPICVTFTTSICAGYC 52

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Oy -----ETWEKPILEPPYIEAHHRVCYYNETKOYTVKLENCAPGYDPFYIYPVAIRDCD 117
      | ::| : ||||| : ::||| ||||| ::||| : |
Db 53 PSMRRLTITARPV---POL-----VCIIYDELRASTIRLPGCPGYDPVVSFPVALSCHC 104
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Db 53 PSMRVLTTARPV---POL----VCTYDELRFASIRLPGCPPGVDPVVSFPVALSCHC 104

QY 118 GACSTATTEC 127

QY 118 GACSIAIIEC 121

Search completed: July 9, 2002, 13:37:17
Job time: 232 sec

Job time: 232 sec